

The period of the Enhanced  
Evolutionary Synthesis  
(from 1950) (Part 2)

## The period of the Enhanced Evolutionary Synthesis (from 1950) (Part 2)

### Exercise 1 (home group, individual work):

Read the following text carefully. Your task is to fill in the missing words and phrases, which you know from your biology lessons. If you need help, you can...

- ...go back in the text or
- ...read further.

If you have problems understanding the text, write down your questions!

In the 1960s, the Japanese scientist **Motoo Kimura** investigated the degree of genetic variance in natural populations. He critically looked at the common assumption that mutations are either disadvantageous or advantageous because it contradicts the possibility of a great number of variations. Kimura applied a method, which enabled him to investigate the variance between individuals on the level of proteins. It turned out that the amino acid sequences of proteins in one population differed more often than previously assumed. Thus, Kimura concluded that most changes in the DNA do not have any influence on the survival and the reproduction rate of an organism. In other words, Kimura found out that most mutations are neutral. In 1968, he published his theory of \_\_\_\_\_ evolution. This discovery did not contradict to the concept of natural selection, but rather added to existing evolutionary concepts. Not every mutation leads to phenotypical changes, which are subject to selection.

Although Watson and Crick had analyzed the structure of DNA in the 1950s, it remained unclear, how this structure encodes information. Theoretical considerations suggested that three nucleotides contribute the information for one amino acid. **Marshall Nirenberg** and **Heinrich Matthaei** first succeeded in 1961 in synthesizing triplets (consisting of three nucleotides) outside a cell. They found out that RNA-triplets consisting of Uracil-nucleotides encode the amino acid phenylalanine. Soon they were able to synthesize RNA-triplets with nucleotide sequences in any combination.

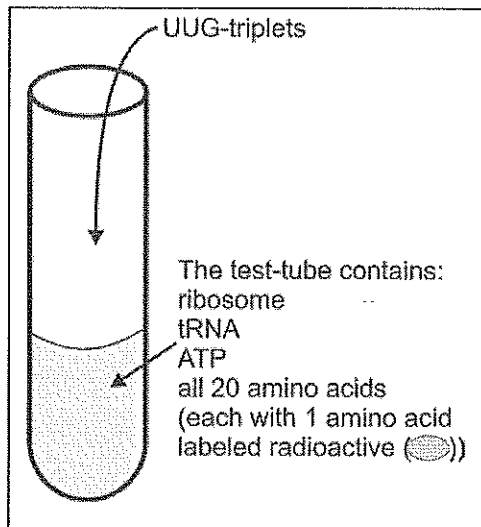


Fig. 1: Illustration of the preparation. A total of 20 test-tubes are filled with the defined components. Each test-tube contains another radioactive labeled amino acid.

The following figures illustrate an experiment for identifying the amino acid which is encoded by the triplet UUG. The preparation for the experiment is shown in figure 1. Then, 20 test-tubes are filled with defined components, with each test-tube containing different radioactively labeled amino acids. The test-tubes are left standing some time, so that the UUG-triplets can attach to the corresponding amino acid and to the ribosome. Afterwards, the main test run starts, composed of a maximum of 20 experiments (see figure 2).

Next, the contents of each test-tube are filtered.

The special filter retains only the ribosome and the attached components. Then, analyses of all 20 test-tubes reveal, in which test-tube radioactively labeled amino acid are retained.

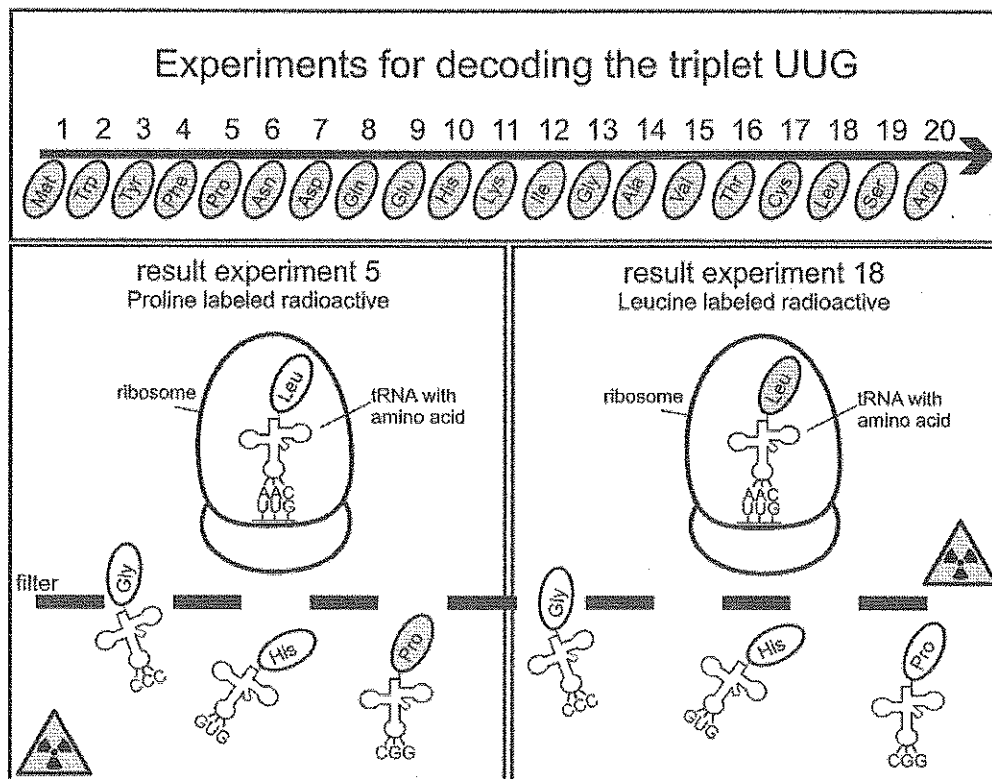


Fig. 2: The course of the test runs by Marshall and Nirenberg using the example of the triplet UUG. Two from a total of 20 experiments are illustrated (see arrow). The content of each test-tube will be filtered.

Nearly at the same time the scientist **Har Gobind Khorana** succeeded in synthesizing longer RNA-fragments outside the cell. Thus, the three scientists gained further insights into the nature of the codons. Thus the whole \_\_\_\_\_ could be decoded in 1966.

The genetecist **Lynn Margulis** rediscovered the \_\_\_\_\_ in 1970. The theory was originally formulated by the Russian Merezhkowsky, who published it in 1910 without attracting further interest. The theory of endosymbiosis explains that chloroplasts and mitochondria of the eukaryotes are descendants from freely living prokaryotes, which entered the host cells through endosymbiosis at some point in the course of evolution.

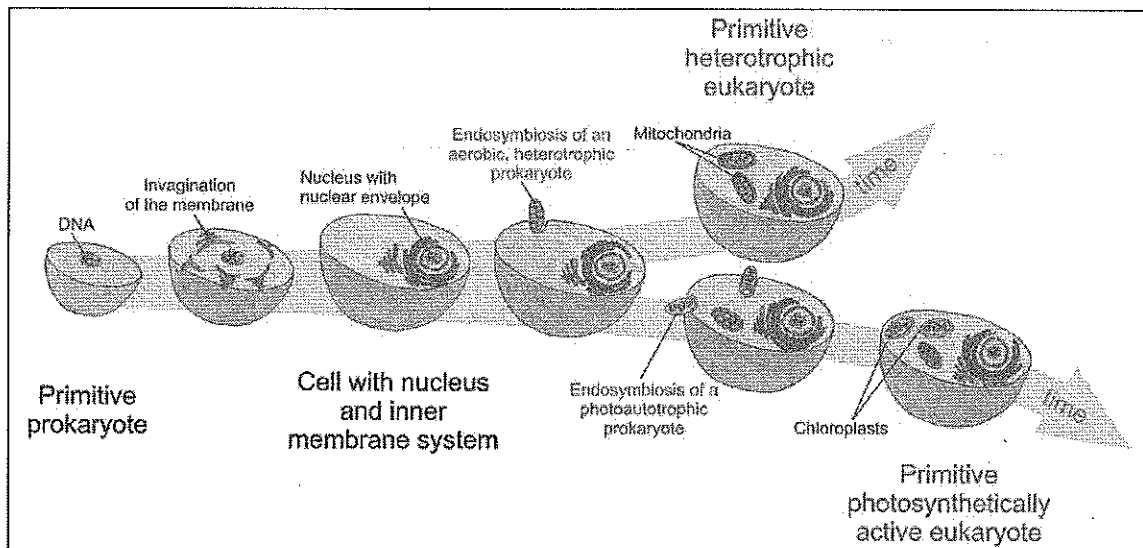


Fig. 3: The theory of endosymbiosis.

In 1977, **Frederick Sanger** developed the method of \_\_\_\_\_ . This method enabled researchers to determine the nucleotide sequence of a DNA molecule. The result is the sequence of the DNA strand which is complementary to the template.

The basis of this method is the random assembly of a modified nucleotide (ddATP, ddCTP, ddTTP or ddGTP) during DNA-replication. It provokes the termination of the synthesis of the amplified strand, because the 3'-OH-end for the attachment of the next nucleotide is lacking. This results in many DNA fragments of different length, which can be separated by size through gel electrophoresis. Radioactive bands can be made visible (fig. 4) through autoradiography.

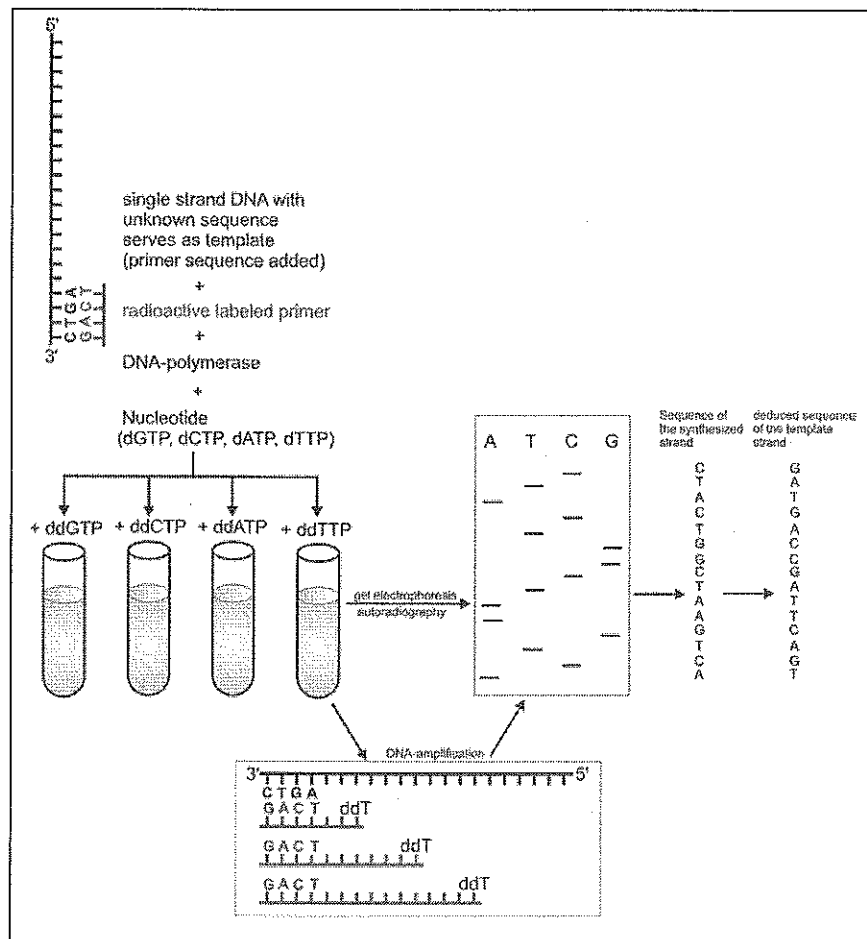


Fig. 4: The method of DNA sequencing according to Frederick Sanger.

Another important step in the further development of evolutionary theory was the integration of the developmental biology, which deals with the development from the zygote to the complete organism. In 1980, the scientists **Edward Lewis**, **Eric Wieschaus** and **Christiane Nüsslein-Volhard** discovered the so called homeotic genes, which control embryonic development. These genes determine where, when and how specific segments of the body, like e.g. eyes or extremities, develop in an organism. Edward Lewis found the first of these genes when he investigated a *Drosophila* mutant bearing two instead of one pair of wings (fig. 5). Meanwhile, \_\_\_\_\_ have been found in many different species. It became clear that particular nucleotide sequences (so-called ‘homeoboxes’) of these genes are identical or very similar in many species.

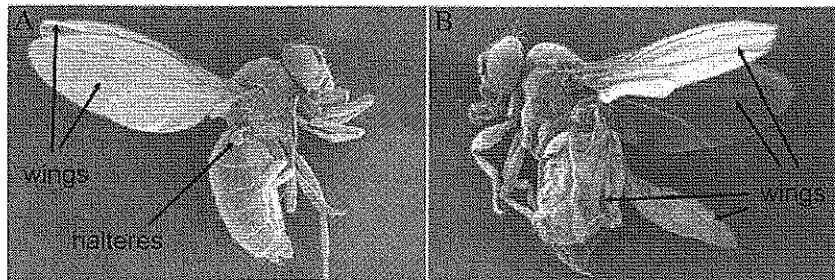


Fig. 5:  
A *Drosophila* wild type  
B *Drosophila* mutant,  
bearing two instead of  
one pair of wings.

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Prof. Dr. Achim Paululat (University of  
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In 1982, **John Maynard Smith** made another important contribution. He applied the game theory, commonly used in economics, in order to explain behavioral patterns from an evolutionary perspective. Often, it can be observed that individuals of a species use different behavioral strategies in identical contexts. The game theory allows for predicting, when alternative behavioral strategies can exist in parallel and when one strategy displaces the other. Strategies, which stand up to alternative behavioral strategies and resist change, are called \_\_\_\_\_ (ESS). By means of applying game theory and identifying evolutionary stable strategies it was possible to explain behavioral strategies, which had hitherto been unable to explain from the perspective of individual selection alone.

### Exercise 2 (expert group, teamwork)

Check your cloze texts and your reading comprehension for correctness. Subsequently answer the following questions:

- a) Because of the nature of the genetic code some point mutations do not result in a different gene product. Use the codon table to find out, at which positions of a nucleotide triplet neutral mutations can occur! Give an example.

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- b) Which amino acid is encoded by the triplet UUG? How did Nirenberg and Matthaei discover this? Explain how the experiment was conducted with the aid of the text and the figures.

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- c) Use figure 3 to explain, how the theory of endosymbiosis explains the formation of cells with mitochondria and chloroplasts.

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- d) Use the example of the fly with two pairs of wings in order to explain the function of homeotic genes.

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**Exercise 3 (expert group, individual work)**

Copy the terms you filled into the gaps of the cloze text (everything that is underlined) onto the 'milestone-cards' (see last page of the material). There is one card for each milestone from the period of the enhanced evolutionary synthesis (part 2).

**Exercise 4 (home group, teamwork):**

Each of you is asked to present the milestones of his/her period to the other team members by attaching the milestone-cards chronologically to the time bar. The expert for the period of Darwinism starts. For each milestone-card, the expert explains, which person arrived at which insight by which means and how the insight changed evolutionary theory. Afterwards, the next expert follows until the time bar is completed.

**Exercise 5 (home group, teamwork):**

After completing the time bar, your team creates a concept map with as many connections as possible.

- 1.) Choose at least 12 milestones from the time bar (each period should be included).
- 2.) Write down the term from each milestone on a piece of paper.
- 3.) Arrange the pieces on a blank sheet so that the milestones which have a close connection lie close to each other. Consider what kind of relationship exists between the different milestones.

**The following advices may help you:**

The relation between two terms can be that ...

- ... one term is an example of the other term (i.e.: mimicry is an example of natural selection).
- ... one term is part of the other term in the sense of a whole – part relationship (i.e.: chromosomes contain genes).
- ... terms are superordinate or subordinate concepts (i.e. mutation and selection are evolutionary factors).



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- 4.) If you are satisfied with the arrangement of the milestones and the relations between them, glue the pieces of paper on the blank sheet.
- 5.) Now draw arrows between the terms.
- 6.) Describe the relationship above the arrows.